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OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:06 ; Search time 244 Seconds
(without alignments)
4876.318 Million cell updates/sec

Title: US-09-840-795-18_COPY_78_770

Perfect score: 693
Sequence: 1 atgagctgcgaagaataatga.....agcagcaggggcctgaatg 693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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- 7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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- 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	100.0	932	21	AA292411
2	685	98.8	3861	22	AA272998
3	668.4	96.5	3152	22	AA278049
4	611.4	88.2	1162	22	AA505944
5	609.4	87.9	899	22	AA633933
6	609.4	87.9	899	22	AA633934
7	593.4	85.6	905	21	AA622332
8	593.4	85.6	905	21	AA658642
9	593.4	85.6	905	22	AA633931

c	10	593.4	85.6	905	22	AA633932	Human TNFR homolog
	11	518	74.7	1550	21	AAA47453	Human TANKO 140-1
	12	446.6	64.4	891	22	AA505960	Degenerate cDNA se
	13	446.4	64.4	807	22	AA505945	Human uterine myom
	14	427.4	61.7	3385	21	AAA47454	Human TANKO 140-2
	15	413.2	59.6	1081	22	AA505973	Expression vector
	16	393.2	56.7	534	22	AA505954	Human soluble ztnf
	17	393.2	56.7	1200	22	AA505955	Human soluble ztnf
	18	317.4	45.8	801	22	AA505961	Degenerate cDNA se
	19	315.4	45.5	519	22	AA505966	Degenerate DNA seq
	20	257	37.1	528	22	AA505962	Poly nucleotide seq
	21	248.2	35.8	546	21	AA292410	cDNA encoding huma
	22	248.2	35.8	546	22	AA28012	Human TNFR homolog
	23	229.6	33.1	474	21	AA292409	cDNA encoding huma
	24	229.6	33.1	474	22	AA28013	Human TNFR homolog
	25	220.4	31.8	529	22	AA505962	Human UMLR polyunc
	26	188	27.1	292	21	AA622325	Nucleotide sequenc
	27	188	27.1	292	22	AA633995	Human TNFR homolog
	28	163.2	23.5	865	21	AA590154	Murine dTroy gene.
	29	163.2	23.5	886	20	AA23414	Mouse MAP04-alpha
	30	163.2	23.5	942	20	AA23414	Mouse TRAF1 (lon
	31	163.2	23.5	981	20	AA23413	Mouse STRIP1 (Tan
	32	163.2	23.5	1678	20	AA23413	Mouse MAP04-alpha
	33	163.2	23.5	1914	22	AA508985	Murine TRAF6 cDNA.
	34	163.2	23.5	4089	21	AA590147	Murine Troy gene.
	35	156.4	22.6	1272	21	AA590148	Human Troy gene.
	36	156.4	22.6	1489	20	AA593415	Human HAPO4-alpha
	37	154.8	22.3	987	20	AA593415	Human NTR-5 cDNA.
	38	154.8	22.3	1254	22	AA590463	Human TNFR homolog
	39	154.8	22.3	1325	22	AA508984	Human TNFR homolog
	40	154.8	22.3	1496	19	AA533362	Nucleotide sequenc
	41	154.8	22.3	1502	20	AA508689	Novel nucleotide s
	42	154.8	22.3	1660	22	AA508983	Human TRAF6-alpha
	43	154.8	22.3	1704	19	AA533361	Nucleotide sequenc
	44	154.8	22.3	2185	20	AA234361	Human TRAF1-R cDNA
	45	154.8	22.3	2870	21	AA586339	Human PRO4333 prot

ALIGNMENTS

RESULT 1	AA292411	standard; cDNA; 932 BP.
ID	AA292411	standard; cDNA; 932 BP.
XX	AA292411	
AC	AA292411	
XX	AA292411	
DT	05-JUN-2000	(first entry)
XX	05-JUN-2000	(first entry)
DE	CDNA encoding human Rank-like protein RANKL, SEQ ID NO:22.	
XX	TNF receptor family; tumour necrosis factor; HDTFA84; HSLJD37R;	
KW	Rank-like protein; RANKL; immune disorder; inflammation; allergy;	
KW	immunosuppressant; antirheumatic; antirheumatoid; antiinflammatory;	
KW	dermatological; antithyroid; ss.	
XX	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	78..773	/tag= a
FT	CDS	/product= "Human RANKL"
FT		
XX	WO200001817-A2.	
PN	13-JAN-2000.	
XX	13-JAN-2000.	
PD	06-JUL-1999;	99WO-US12366.
PF	06-JUL-1998;	98US-0110938.
XX	13-JUL-1998;	98US-0114466.
PR	23-JUL-1998;	98US-0093897.
PR	12-AUG-1998;	98US-0132968.

PR 18-AUG-1998; 9805-0136214.
PR 11-SEP-1998; 9805-00999999.
XX
PA (SCHE) SCHERING CORP.
PI Bates EM, Lebecque SE, Murphy EE, Mattson JD, Gorman DM;
PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
PI Bazan JF, Mahony D, Lees EM;
XX
XX WPI: 2000-171015/15.
DR P-PSDB; AAF77468.
PT New isolated mammalian genes, used to develop products for treating
PT e.g. immune, inflammatory or allergic abnormalities, cancers or
PT degenerative conditions
XX
XX
PS Claim 25; Page 176-177; 218pp; English.
XX
XX The invention relates to a number of primate and/or rodent proteins, and
CC the genes which encode them. The invention encompasses human dendritic
CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis
CC factor) receptor family-related proteins HOTEAR4, HSLUD37R and RANKL;
CC human CC chemokine HCC5; human dendritic proteins Dubil and Dub
CC 12; human MD-1 and human and murine MD-2 proteins, which exhibit the
CC properties of ligands for proteins comprising a leucine-rich motif
CC (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies
CC against these proteins. The proteins can be used for modulating the
CC physiology or development of a cell. They can be used to mediate uptake
CC of substrates (e.g., prostaglandin-like molecules), to modulate or
CC mediate cellular interactions (e.g., induce or prevent trafficking,
CC proliferation, or differentiation of cells), or are intracellular
CC proteins which are important in various cellular processes such as the
CC deubiquitination of proteins or cell cycle regulation. The products can
CC be used for treating medical conditions such as immune, inflammatory or
CC allergic disorders, or abnormal cellular proliferation, for example,
CC cancers or degenerative conditions. They can be used to modulate immune
CC responses in disease states e.g., autoimmune disorders, including
CC rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
CC autoimmune thyroiditis, as well as acute and chronic inflammatory
CC responses in which T cell activation, expansion, and/or immunological T
CC cell memory play an important role. Sequences AA92404-92411 represent
CC cDNAs encoding TNF receptor family-related proteins. AA92404 encodes the
CC human protein HOTEAR4, AA92405-92407 encode human HSLUD37R proteins,
CC AA92408 encodes murine Rank-like protein RANKL, and AA92409-92411
CC encode human RANKL proteins.
XX
XX
SQ Sequence 932 BP; 205 A; 260 C; 246 G; 220 T; 1 other:

Query Match 100.0%; Score 693; DB 21; Length 932;
Best Local Similarity 100.0%; Pred. No. 6.9e-198;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 378 GACCAAGATGATCCCGTGGACAGACAGACACCCACCTCTGAGATTCAATGTCCTTC 437
|||
QY 361 CAGTTGAGCTTAGTGAGAGCAGATGCACCCACAGTGCCTCCAGAGGCCACACTTGT 420
|||
DB 438 CAGTTGAGCTTAGTGAGAGCAGATGCACCCACAGTGCCTCCAGAGGCCACACTTGT 497
|||
QY 421 GCACGAGTGCAGAGCCTCTAGTGTGTTTACCTTGCCCTTCTTGAGGCTCTTCTCCTC 480
|||
DB 498 GCACGAGTGCAGAGCCTCTAGTGTGTTTACCTTGCCCTTCTTGAGGCTCTTCTCCTC 557
|||
QY 481 TACTGCAACAGATTTCTTAACAGATTCGACGCTTGAGGTTTCTCAGTTGAGCT 540
|||
DB 558 TACTGCAACAGATTTCTTAACAGATTCGACGCTTGAGGTTTCTCAGTTGAGCT 617
|||
QY 541 GATTAACAGCAAGAGAGATCTCTTCCCGTGCCAGCCAGCAAGACAGTGTCT 600
|||
DB 618 GATTAACAGCAAGAGAGATCTCTTCCCGTGCCAGCCAGCAAGACAGTGTCT 677
|||
QY 601 GAGTCCCAAGTCTCTTGGGCCCTGGCAGCTTGCCAGTTGTTCTCTGAGCTGTG 660
|||
DB 678 GAGTCCCAAGTCTCTTGGGCCCTGGCAGCTTGCCAGTTGTTCTCTGAGCTGTG 737
|||
QY 661 CCTATACCAACAAGCAGCAGAGGAGGCTGAATG 693
|||
DB 738 CCTATACCAACAAGCAGCAGAGGAGGCTGAATG 770
|||

RESULT 2
AAF27998
ID AAF27998 standard; DNA; 3861 BP.
XX
AC AAF27998;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human TR14 receptor coding sequence SEQ ID NO: 4.
XX
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.
XX
OS Homo sapiens.
XX
PN WO200105834-A1.
XX
PD 25-JAN-2001.
XX
PE 14-JUL-2000; 2000WO-US19343.
XX
PR 16-JUL-1999; 9905-0144087.
PR 18-AUG-1999; 9905-0149450.
PR 20-AUG-1999; 9905-0149712.
PR 10-SEP-1999; 9905-0153089.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, NI J, Young PE;
XX
DR WPI: 2001-112682/12.
DR P-PSDB; AAB35330.
PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides (TR13) and (TR14), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX
XX Example 7; Page 373-376; 418pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX human tumour necrosis factor receptors TR13 and TR14. These sequences are
XX useful in the diagnosis and treatment of many diseases, including cancer,
XX autoimmune diseases, cardiovascular disorders, allergies,

CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.

XX Sequence 3861 BP; 992 A; 929 C; 860 G; 1071 T; 9 other:

Query Match 98.8%; Score 685; DB 22; Length 3861;
Best Local Similarity 99.3%; Pred. No. 3.3e-195;
Matches 688; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGATTTGCCAAGAAATGACTAGTGGACCAATGGGGAGCGTGTGCTACCTGCCAAGCG 60
DB 3166 ATGATTTGCCAAGAAATGACTAGTGGACCAATGGGGAGCGTGTGCTACCTGCCAAGCG 3225
QY 61 TGTGTCTCTGACAGAGAGTATCCAAAGATTGTTATGAGAGGGTGGAGATGCTAC 120
DB 3226 TGTGTCTCTGACAGAGAGTATCCAAAGATTGTTATGAGAGGGTGGAGATGCTAC 3285
QY 121 TGCACAGCCTGCCCTCTCGCAGGTACAAAAGCAGCTGGGGCCACCAAAATGTCAAGT 180
DB 3286 TGCACAGCCTGCCCTCTCGCAGGTACAAAAGCAGCTGGGGCCACCAAAATGTCAAGT 3345
QY 181 TGCATACCTGTGCTGTCTCATCAATGCTTTGACAGAGTCACTGCACAGCTACTTAAT 240
DB 3346 TGCATACCTGTGCTGTCTCATCAATGCTTTGACAGAGTCACTGCACAGCTACTTAAT 3405
QY 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACGAAAGACAGCAATTGGAGGCTGACAG 300
DB 3406 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACGAAAGACAGCAATTGGAGGCTGACAG 3465
QY 301 GACCAAGAGTGCATCCCGTGCACAGAGACCCCGCAGCTGTGAGGTTCAATGTGCTTC 360
DB 3466 GACCAAGAGTGCATCCCGTGCACAGAGACCCCGCAGCTGTGAGGTTCAATGTGCTTC 3525
QY 361 CAGTTAGCTTATGAGAGCAGATGCACCCACAGTGCCTCCCTCAGAGGCCACACTTGT 420
DB 3526 CAGTTAGCTTATGAGAGCAGATGCACCCACAGTGCCTCCCTCAGAGGCCACACTTGT 3585
QY 421 GCACGTGTGAGCAGCTGTGAGTGTGTTTACCTGCGCTTCTGGGGCTCTTCTCC 480
DB 3586 GCACGTGTGAGCAGCTGTGAGTGTGTTTACCTGCGCTTCTGGGGCTCTTCTCC 3645
QY 481 TACTGCAAGCAGTTCTTCAACAGACATTCGACCGTGAAGGTTTGTGCAAGTTGAGGCT 540
DB 3646 TACTGCAAGCAGTTCTTCAACAGACATTCGACCGTGAAGGTTTGTGCAAGTTGAGGCT 3705
QY 541 GATTAACAGCAAGAGAGATCTCTTCCCGTCCACCCAGCAAGAGAGACAGTGTCT 600
DB 3706 GATTAACAGCAAGAGAGATCTCTTCCCGTCCACCCAGCAAGAGAGACAGTGTCT 3765
QY 601 GAGTCCAGTGTCTTGGGGCCCTGGCAGCTTGGCCAGTGTCTCTGAGACTGT 660
DB 3766 GAGTCCAGTGTCTTGGGGCCCTGGCAGCTTGGCCAGTGTCTCTGAGACTGT 3825
QY 661 CCTATACCAACAGCAGCAGGGGCTGAATG 693
DB 3826 CCTATACCAACAGCAGCAGGGGCTGAATG 3858

RESULT 3

AAF28049 standard; DNA; 3152 BP.

AAF28049;

08-MAY-2001 (first entry)

Human TR14 coding sequence SEQ ID NO: 60.

XX Human: tumour necrosis factor receptor; TR13; TR14; infection;
XX Human: autoimmune disease; allergy; inflammatory disease;
XX graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.
OS Homo sapiens.

XX MO200105834-A1.

XX 25-JAN-2001.

XX 14-JUL-2000; 2000MO-US19343.

XX 16-JUL-1999; 99US-0144087.

XX 18-AUG-1999; 99US-0149450.

XX 20-SEP-1999; 99US-0149712.

XX 10-SEP-1999; 99US-0153089.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J, Young PE;

XX WPI: 2001-112682/12.

XX P-PSDB; AAB35335.

XX Nucleic acids encoding 2 human tumor necrosis factor receptor

XX polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis

XX and treatment of, e.g., cancers, acquired immune deficiency syndrome and

XX hypohidrotic ectodermal dysplasia -

XX Claim 6; Page 412-413; 418pp; English.

XX The present invention provides the protein and coding sequences of the

XX human tumour necrosis factor receptors TR13 and TR14. These sequences are

XX useful in the diagnosis and treatment of many diseases, including cancer,

XX autoimmune diseases, cardiovascular disorders, allergies,

XX neurodegenerative diseases, graft rejection, inflammation, aneurysms and

XX infections.

XX Sequence 3152 BP; 840 A; 739 C; 663 G; 908 T; 2 other:

Query Match 96.5%; Score 668.4; DB 22; Length 3152;
Best Local Similarity 99.6%; Pred. No. 2.9e-190;
Matches 691; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATGATTTGCCAAGAAATGAGTACTGGACCAATGGGAGCGTGTGCTACCTGCCAAGCG 60
DB 67 ATGATTTGCCAAGAAATGAGTACTGGACCAATGGGAGCGTGTGCTACCTGCCAAGCG 126
QY 61 TGTGTCTCTGACAGAGAGCTATCCAAAGATTGTTATGAGAGGGTGGAGATGCTTAC 120
DB 127 TGTGTCTCTGACAGAGAGCTATCCAAAGATTGTTATGAGAGGGTGGAGATGCTTAC 186
QY 121 T-GCAGAGCCTGCCCTCCCTGCGAGGTACAAAGACAGCTGGGGCCACCAAAATGTCAGAG 179
DB 187 TGGCAGAGCCTGCCCTCCCTGCGA-GTACAAAGACAGCTGGGGCCACCAAAATGTCAGAG 245
QY 180 TTGCATCACCTGTGCTGTCTCATCAATGCTGTTCAAGAGTTCACATGCACTACTCTAA 239
DB 246 TTGCATCACCTGTGCTGTCTCATCAATGCTGTTCAAGAGTTCACATGCACTACTCTAA 305
QY 240 TGTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGGCTGCA 299
DB 306 TGTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGGCTGCA 365
QY 300 GGACCAAGAGTGCATCCCGTGCAGAGCAGACCCCACTCTGAGGTTCAATGTGCTT 359
DB 366 GGACCAAGAGTGCATCCCGTGCAGAGCAGACCCCACTCTGAGGTTCAATGTGCTT 425
QY 360 CCAAGTTAGCTTATGAGAGCAGATGCACCAAGTGGCCCTCAGAGAGGCCACACTTGT 419
DB 426 CCAAGTTAGCTTATGAGAGCAGATGCACCAAGTGGCCCTCAGAGAGGCCACACTTGT 485
QY 420 TGCATGTGTGAGAGAGCTGTATGTGTTTACCCTTGCCCTTCTGGGGCTCTTCTTCC 479
DB 486 TGCATGTGTGAGAGAGCTGTATGTGTTTACCCTTGCCCTTCTGGGGCTCTTCTTCC 545
QY 480 CTACTGCAAGCACTTCTTCAACAGACATTGCGAGCGGTGCTGCTGACGTTGAGGC 539

Db 546 CTATGCAAGACGTTCTTCAACAGACATTGCCAGCGTGAGGTTGCTGACGTTTGAGGC 605
OY 540 TGATATAACAGCAAGAGCAATCTCTTCCCGTGCCAGCCAGCAAGAGACAGTGC 599
Db 606 TGATATAACAGCAAGAGGAAATCTCTTCCCGTGCCAGCCAGCAAGAGACAGTGC 665
OY 600 TGAGTCCCAAGTCTTGGGCCCCGTGGACAGCCTTGCCAGTTGTTCTCTGAGCTCTGT 659
Db 666 TGAGTCCCAAGTCTTGGGCCCCGTGGACAGCCTTGCCAGTTGTTCTCTGAGCTCTGT 725
OY 660 TCCTATACCAACAGCAAGGAGGCGCTGAATG 693
Db 726 TCCTATACCAACAGCAAGGAGGCGCTGAATG 759

RESULT 4
AAS05944
ID AAS05944 standard; cDNA: 1162 BP.
AC AAS05944;
XX
XX 07-SEP-2001 (first entry)
DE Human uterine myometrium leiomyoma receptor (UMLR) cDNA sequence.
XX
XX Human; uterine myometrium leiomyoma receptor; UMLR; ztnf11;
KW tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
XX gene therapy; ss.
OS Homo sapiens.
XX
FH Location/Qualifiers
FT CDS 104..913
FT /*tag= a
FT /product= "UMLR"
FT /note= "Also known as ztnf11"
XX
XX MO200130850-A1.
XX
XX 03-MAY-2001.
PD 23-0CT-2000; 2000WO-US29304.
XX
XX 22-0CT-1999; 99US-0160880.
PR 02-NOV-1999; 99US-0163215.
PR 17-JUL-2000; 2000US-0218769.
PR 01-AUG-2000; 2000US-0222221.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Xu W, Lofton-Day CE, Henne R, Presnell SR, Yao Y, Novak JE;
PI Foster DC, Yee DP;
XX
XX WPI: 2001-300488/31.
DR P-PSDB; AAU03106.
XX
XX uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT for modulating inflammation, tumour growth, metastasis, cellular
PT maturation, detecting modulators and as diagnostic indicators of cancer
PT
XX
XX Claim 9; Page 114-116; 148BP; English.
XX
XX The present sequence encoding for a novel human uterine myometrium
CC leiomyoma receptor (UMLR) is a member of the tumour necrosis factor
CC receptor (TNFR) family. The UMLR (also known as ztnf11) gene maps to
CC chromosome Xq11-q12. Amino acid residues of UMLR involved in ligand
CC binding, consisting of residues 1-X (where X is 129-136) are useful
CC for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC or its fragments are useful diagnostically or therapeutically for
CC identifying tumour cells in uterus melanoma and lung cancer, for

CC promoting wound healing, and for generating vaccines for cancer therapy.
CC They are also useful for studying cell-cell interactions, apoptosis,
CC fertilisation, development, immune recognition, growth control, tumour
CC suppression and embryo maturation in vitro and in vivo, and for treating
CC disorders associated with them. UMLR is also useful for identifying
CC inhibitors of its activity, and for preparing antibodies which can be
CC used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC as probes or primers as diagnostic indicators of cancer and for gene
CC therapy.
XX
XX Sequence 1162 BP; 255 A; 327 C; 314 G; 266 T; 0 other;
SQ
Query Match 88.2%; Score 611.4; DB 22; Length 1162;
Best Local Similarity 99.0%; Pred. No. 2.4e-173;
Matches 615; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 ATGATTTGCCAAGAAATGACTGTGGACCAATGGGAGCGTGTGACCTGCCAACGG 60
Db 104 ATGATTTGCCAAGAAATGACTGTGGAGCAATGGGAGCGTGTGACCTGCCAACGG 163
OY 61 TGTGTCCTGGACAGAGACTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 120
Db 164 TGTGTCCTGGACAGAGACTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 223
OY 121 TGACAGAGCCTGCTCCTCTGCGAGATGACAAAGACAGCTGGGCCACACAAATGTGAGAGT 180
Db 224 TGACAGAGCCTGCTCCTCTGCGAGATGACAAAGACAGCTGGGCCACACAAATGTGAGAGT 283
OY 181 TGCAATCACCTTGCTGTGTATCATATGCTGTTCAGAAAGTCAAGTGCACAGTACCTTAAT 240
Db 284 TGCAATCACCTTGCTGTGTATCATATGCTGTTCAGAAAGTCAAGTGCACAGTACCTTAAT 343
OY 241 GGTGTCCTGGGAGCTGTTGGCCAGGTTTCACGAAAGACAGATGGAGGCGCTGAG 300
Db 344 GGTGTCCTGGGAGCTGTTGGCCAGGTTTCACGAAAGACAGATGGAGGCGCTGAG 403
OY 301 GACCAAGAGTGCATCCCTGCGACGAGACAGACCCCACTCTGAGGTTCATATGTGCTTC 360
Db 404 GACCAAGAGTGCATCCCTGCGACGAGACAGACCCCACTCTGAGGTTCATATGTGCTTC 463
OY 361 CAGTTGACCTTAGTGGAGGACGATGACCCACAGTGCCTCAGAGAGGCCACACTTGT 420
Db 464 CAGTTGACCTTAGTGGAGGACGATGACCCACAGTGCCTCAGAGAGGCCACACTTGT 523
OY 421 GCACGTGGAGCAGGCTCTAGTGTGTTTACCGTGGGCTTCGAGGCTCTTCTTC 480
Db 524 GCACGTGGAGCAGGCTCTAGTGTGTTTACCGTGGGCTTCGAGGCTCTTCTTC 583
OY 481 TACTGCAAGAGTCTTTCACAGACATTGCCAGGTGAGGTTGCTGCACTTTGAGGCT 540
Db 584 TACTGCAAGAGTCTTTCACAGACATTGCCAGGTGAGGTTGCTGCACTTTGAGGCT 643
OY 541 GATATAACAGCAAGAGGAAATCTCTTCCCGTGCCAGCCAGCAAGAGACCAAGTCT 600
Db 644 GATATAACAGCAAGAGGAAATCTCTTCCCGTGCCAGCCAGCAAGAGACCAAGTCT 703
OY 601 GAGTCCCAAGTCTCTGGGCC 621
Db 704 GAGTCCCAAGTCTCTTTACC 724

RESULT 5
AAC63993
ID AAC63993 standard; cDNA: 899 BP.
XX
XX AAC63993;
AC
XX 14-FEB-2001 (first entry)
DT
XX
XX Human TNFR homologue clone DNA101848 cDNA.
DE
XX
XX Human; TNFR homologue; tumour necrosis factor receptor; DNA101848;
KW apoptosis; NF-kappa-B activation; proinflammatory response;

KM autoimmune response; modulation; antibody; EDA-A2 inhibition;
 KW gene mapping; antisense therapy; gene therapy; ATCC 203907; ss.
 XX Homo sapiens.
 OS
 PN W0200061757-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000MO-US09699.
 XX
 PR 12-APR-1999; 99US-0128849.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Goddard A, Pan J, Yan M;
 XX
 DR WPI: 2001-070561/08.
 DR P-PSDB; AAB29534.
 XX
 PT New isolated nucleic acid encoding a tumor necrosis factor homolog for
 PT modulating apoptosis, NF-kappaB activation, pro-inflammatory or
 PT autoimmune response in mammalian cells -
 PS
 PS Claim 27; Fig 3; 82pp; English.
 XX
 CC The invention relates to the human tumour necrosis factor receptor
 CC (TNFR) homologues DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
 CC encoding them (AAC63991, AAC63993), and to the complements (AAC63992,
 CC AAC63994) of nucleic acids encoding the TNFR homologues. The invention
 CC also relates to vectors and host cells comprising DNA98853 or DNA101848
 CC nucleic acids, fusion proteins comprising the DNA98853 or DNA101848
 CC proteins, antibodies against the DNA98853 or DNA101848 proteins,
 CC recombinant expression of the DNA98853 or DNA101848 proteins. The
 CC invention further encompasses a method of modulating apoptosis,
 CC NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
 CC autoimmune response using the DNA98853 or DNA101848 proteins, and a
 CC method of inhibiting or neutralising EDA-A2 protein biological activity
 CC in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
 CC DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
 CC NF-kappa-B activation, proinflammatory or autoimmune responses in
 CC mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
 CC antibodies) can be used to inhibit or neutralise EDA-A2 protein
 CC biological activity in mammalian cells. DNA98853 and DNA101848
 CC nucleic acids can be used as hybridisation probes in chromosome and gene
 CC mapping, in the generation of antisense RNA and DNA, and in gene
 CC therapy. The present sequence represents cDNA encoding DNA101848 (ATCC
 CC 203907).
 CC
 XX
 SQ Sequence 899 BP; 208 A; 259 C; 239 G; 193 T; 0 other;
 Query Match 87.9%; Score 609.4; DB 22; Length 899;
 Best Local Similarity 99.8%; Pred. No. 8..7e-173;
 Matches 610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 244 GCTGTCGTGGGAGCATGTTGCCAGGTTCTACCCGAAAGACAGCATTTGAGCGCTCGAG 303
 QY 301 GACCAAGATGTCATCCGTCGACAGACAGACCCACCTTGAGTTCAATGTGCCCTTC 360
 Db 304 GACCAAGATGTCATCCGTCGACAGACAGACCCACCTTGAGTTCAATGTGCCCTTC 363
 QY 361 CAGTTGAGCTTAGTGGAGGCGATGACCCCACTGGCCCCCTCGAGAGGCCACACTTGT 420
 Db 364 CAGTTGAGCTTAGTGGAGGCGATGACCCCACTGGCCCCCTCGAGAGGCCACACTTGT 423
 QY 421 GCACGTGTGAGCAGCCTGCTAGTGTGTTTACCTGGCCTTCTCGGGCTTTCTTCCTC 480
 Db 424 GCACGTGTGAGCAGCCTGCTAGTGTGTTTACCTGGCCTTCTCGGGCTTTCTTCCTC 483
 QY 481 TACTGCAAGCAGTTCTTCAACAGACATTCGAGCGAGGTTTGTCTGCACTTTGAGGCT 540
 Db 484 TACTGCAAGCAGTTCTTCAACAGACATTCGAGCGAGGTTTGTCTGCACTTTGAGGCT 543
 QY 541 GATTAACAGCAAGAGGAGATCTCTCTCCCGTGGCACCAGCAGAGAGACCACTGCT 600
 Db 544 GATTAACAGCAAGAGGAGATCTCTCTCCCGTGGCACCAGCAGAGAGACCACTGCT 603
 QY 601 GAGTCCCAAGT 611
 Db 604 GAGTCCCAAGT 614
 RESULT 6
 AAC63994/c
 ID AAC63994 standard; cDNA; 899 BP.
 XX
 AC AAC63994:
 DT 14-FEB-2001 (first entry)
 XX
 DE Human TNFR homologue clone DNA101848 cDNA complement.
 XX
 KW Human; TNFR homologue; tumour necrosis factor receptor; DNA101848;
 KW apoptosis; NF-kappa-B activation; proinflammatory response;
 KW autoimmune response; modulation; antibody; EDA-A2 inhibition;
 KW gene mapping; antisense therapy; gene therapy; ATCC 203907; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200061757-A1.
 PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000MO-US09699.
 XX
 PR 12-APR-1999; 99US-0128849.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Goddard A, Pan J, Yan M;
 XX
 DR WPI: 2001-070561/08.
 DR P-PSDB; AAB29534.
 XX
 PT New isolated nucleic acid encoding a tumor necrosis factor homolog for
 PT modulating apoptosis, NF-kappaB activation, pro-inflammatory or
 PT autoimmune response in mammalian cells -
 PS
 PS Claim 27; Fig 3; 82pp; English.
 XX
 CC The invention relates to the human tumour necrosis factor receptor
 CC (TNFR) homologues DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
 CC encoding them (AAC63991, AAC63993), and to the complements (AAC63992,
 CC AAC63994) of nucleic acids encoding the TNFR homologues. The invention
 CC also relates to vectors and host cells comprising DNA98853 or DNA101848
 CC nucleic acids, fusion proteins comprising the DNA98853 or DNA101848
 CC proteins, antibodies against the DNA98853 or DNA101848 proteins. The
 CC recombinant expression of the DNA98853 or DNA101848 proteins. The

CC invention further encompasses a method of modulating apoptosis,
CC NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
CC autoimmune response using the DNA98853 or DNA101848 proteins, and a
CC method of inhibiting or neutralising EDA-A2 protein biological activity
CC in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
CC DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
CC NF-kappa-B activation, proinflammatory or autoimmune responses in
CC mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
CC antibodies) can be used to inhibit or neutralise EDA-A2 protein
CC biological activity in mammalian cells. DNA98853 and DNA101848
CC nucleic acids can be used as hybridisation probes in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, and in gene
CC therapy. In the present sequence represents the complement of cDNA encoding
CC DNA101848 (ATCC 203907).

CC
XX
SQ Sequence 899 BP; 193 A; 239 C; 259 G; 208 T; 0 other;

Query Match 87.9%; Score 609.4; DB 22; Length 899;
Best Local Similarity 99.8%; Pred. No. 8.7e-173;

Matches 610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 ATGGATTGCCAAGAAATAGTACTGGGACCAATGGGGAGGCTGTGTCACCTGCCACGG 60
DB 896 ATGGATTGCCAAGAAATAGTACTGGGACCAATGGGGAGGCTGTGTCACCTGCCACGG 837
OY 61 TGTGTCTCGACAGAGAGCTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 120
DB 836 TGTGTCTCGACAGAGAGCTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 777
OY 121 TGCACAGCCTGCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACCAAAATGTGAGAGT 180
DB 776 TGCACAGCCTGCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACCAAGATGTGAGAGT 717
OY 181 TGCATCACCCTGTGCTCATCATGTGTTCAGAGGTCAACTGCACAGCTACCTCTAAT 240
DB 716 TGCATCACCCTGTGCTCATCATGTGTTCAGAGGTCAACTGCACAGCTACCTCTAAT 657
OY 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGGCTGCAG 300
DB 656 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGGCTGCAG 597
OY 301 GACCAAGATGATCCCTGCGACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTC 360
DB 596 GACCAAGATGATCCCTGCGACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTC 537
OY 361 CAGTTGAGCTTGTAGTGAGAGATGACACCAAGTGCCTCCCTCAGAGGCCACACTTGT 420
DB 536 CAGTTGAGCTTGTAGTGAGAGATGACACCAAGTGCCTCCCTCAGAGGCCACACTTGT 477
OY 421 GCACGTGTGAGCAGCTCTCTAGTGTGTTTACCTGGCCTTCTGCGGCTCTTCTTCCTC 480
DB 476 GCACGTGTGAGCAGCTCTCTAGTGTGTTTACCTGGCCTTCTGCGGCTCTTCTTCCTC 417
OY 481 TACTCAGAGAGCTCTTCAACAGATGCGACAGCTGAGAGTTTCTCTCAGTTTAGGCT 540
DB 416 TACTCAGAGAGCTCTTCAACAGATGCGACAGCTGAGAGTTTCTCTCAGTTTAGGCT 357
OY 541 GATAAAGACGAAAGAGGAATCTCTTCCCGTGCACCCAGCAGAGAGAGACCGAGTCT 600
DB 356 GATAAAGACGAAAGAGGAATCTCTTCCCGTGCACCCAGCAGAGAGAGACCGAGTCT 297
OY 601 GAGTCCCAAGT 611
DB 296 GAGTCCCAAGT 286
```

RESULT 7

AAC62232
ID AAC62232 standard; cDNA; 905 BP.

XX AAC62232;
AC
XX

DT 06-MAR-2001 (first entry)

XX
DE cDNA encoding a human DNA98853 polypeptide.

XX
KW Human; DNA58893; full length inverse polymerase chain reaction; FLIP;
KW Inverse long distance PCR; ds.

XX
OS Homo sapiens.

PH Key Location/Qualifiers
FT CDS 4..303
FT /tag= a
FT /product= "DNA98853"

PN WO20061741-A1.

PD 19-OCT-2000.

PF 10-APR-2000; 2000WO-US09554.

PR 12-APR-1999; 99US-0128849.

PR 10-JAN-2000; 2000US-0480782.

PA (GETH) GENENTECH INC.

PI Chui CJ, Grimaldi JC, Milton S, Yan M, Yi S;

DR WPJ: 2000-679484/66.

DR P-PSDB; AAB30547.

XX
XX
XX New polymerase chain based cloning method for isolating a nucleic acid
PT molecule of interest from a mixture of nucleic acid molecules using
PT full length inverse PCR -

XX
XX
XX Example 2; Fig 4; 31pp; English.

XX
XX
XX The present sequence encodes a human DNA98853 polypeptide. The
CC DNA98853 gene was amplified and cloned using a PCR-based method of
CC the invention, called full length inverse polymerase chain reaction
CC (FLIP). FLIP is also referred to as inverse long distance PCR,
CC because of its ability to isolate long genes. The specification uses
CC FLIP for amplifying and isolating a nucleic acid molecule of interest
CC from a mixture of nucleic acid molecules. The method is useful for
CC efficiently cloning a wide variety of genes.

XX
SQ Sequence 905 BP; 210 A; 260 C; 240 G; 195 T; 0 other;

Query Match 85.6%; Score 593.4; DB 21; Length 905;
Best Local Similarity 98.9%; Pred. No. 5.5e-168;

Matches 610; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

```
OY 1 ATGGATTGCCAAGAAATAGTACTGGGACCAATGGGGAGGCTGTGTCACCTGCCACGG 60
DB 4 ATGGATTGCCAAGAAATAGTACTGGGACCAATGGGGAGGCTGTGTCACCTGCCACGG 63
OY 61 TGTGTCTCGACAGAGAGCTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 120
DB 64 TGTGTCTCGACAGAGAGCTATCCAAAGATGTGTTATGAGAGAGGTGAGATGCCCTAC 123
OY 121 TGCACAGCCTGCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACCAAAATGTGAGAGT 180
DB 124 TGCACAGCCTGCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACCAAGATGTGAGAGT 183
OY 181 TGCATCACCCTGTGCTCATCATGTGTTCAGAGGTCAACTGCACAGCTACCTCTAAT 240
DB 184 TGCATCACCCTGTGCTCATCATGTGTTCAGAGGTCAACTGCACAGCTACCTCTAAT 243
OY 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGAGGCTTCAG 300
DB 244 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGAGGCTTCAG 303
OY 301 GACCAAGATGATCCCTGCGACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTC 360
DB 304 GACCAAGATGATCCCTGCGACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTC 363
```

Qy	361	CATTGACCTTAGTGGAGGCGAGATGACACCCACCACTGCCCCCTCAGAGGGCCACACTTGT	420
Db	364	CAGTTGACCTTAGTGGAGGCGAGATGACACCCACCACTGCCCCCTCAGAGGGCCACACTTGT	423
Qy	421	GCACGTGGAGACACCTGCTAGTGGTGTTCACCTGGCCCTTCCGAGGGCTCTTCTTCCTC	480
Db	424	GCACGTGGAGACACCTGCTAGTGGTGTTCACCTGGCCCTTCCGAGGGCTCTTCTTCCTC	483
Qy	481	TACTGCGAAGCAGTTCTTCAACAGACACTTGGCCAGCGT-----GGAGTTTGGTCGACGTTT	534
Db	484	TACTGCGAAGCAGTTCTTCAACAGACACTTGGCCAGCGTGTACAGAGGATTGGTCGACGTTT	543
Qy	535	GAGCGCTGATAAAGACGAAGAAGATTCCTCTTCCCGCTGGCACCCACACAGAGAGACC	594
Db	544	GAGCGCTGATAAAGACGAAGAAGATTCCTCTTCCCGCTGGCACCCACAGAGAGACC	603
Qy	595	AGTGCTGAGTCCCAAGT 611	
Db	604	AGTGCTGAGTCCCAAGT 620	

RESULT 8
AAC58642
ID AAC58642 standard; cDNA: 905 BP.
XX
AC AAC58642:
DT 29-JAN-2001 (first entry)
XX
DE Human PRO5727 protein UNQ2448 encoding cDNA SEQ ID NO:296.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiac;
KW dermatological; antifibrillic; antihemetic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; neutrotropic; neuroprotective;
KW antineumatic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW idiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; SS.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PE 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99MO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123657.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99MO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99MO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99MO-US20111.
PR 08-SEP-1999; 99MO-US20594.
PR 13-SEP-1999; 99MO-US20944.
PR 15-SEP-1999; 99MO-US21090.

PR	15-SEP-1999;	99WO-US21547.
PR	05-OCT-1999;	99WO-US23089.
PR	29-OCT-1999;	99US-0162506.
PR	30-NOV-1999;	99WO-US28214.
PR	30-NOV-1999;	99WO-US28213.
PR	30-NOV-1999;	99WO-US28409.
PR	01-DEC-1999;	99WO-US28301.
PR	01-DEC-1999;	99WO-US28634.
PR	02-DEC-1999;	99WO-US28851.
PR	02-DEC-1999;	99WO-US28564.
PR	02-DEC-1999;	99WO-US28565.
PR	16-DEC-1999;	99WO-US30095.
PR	20-DEC-1999;	99WO-US30999.
PR	30-DEC-1999;	99WO-US31274.
PR	05-JAN-2000;	2000WO-US00219.
PR	06-JAN-2000;	2000WO-US00277.
PR	11-FEB-2000;	2000WO-US00376.
PR	11-FEB-2000;	2000WO-US03565.
PR	18-FEB-2000;	2000WO-US04341.
PR	18-FEB-2000;	2000WO-US04342.
PR	22-FEB-2000;	2000WO-US04414.

Claim 23: Fig 127; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAC33414 to AAC33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 905 BP; 210 A; 260 C; 240 G; 195 T; 0 other;

Query Match	85.68;	Score 593.4;	DB 21;	Length 905;
Best Local Similarity	98.98;	Pred. No. 5.5e-168;		
Matches 610; Conservative	0;	Mismatches 1;	Indels 6;	Gaps 1;

QY	1	ATGATTTGCCAAGAAATAGTACTGGACCAATGGGAGCGGTGTGTACCTGCGCAAGG	60
	4	ATGATTTGCCAAGAAATAGTACTGGACCAATGGGAGCGGTGTGTACCTGCGCAAGG	63
QY	61	TGTGTCCTCGACAGAGACTTCCACAGATTTGTGTTATGACAGAGGGTGGAGATCCCTAC	120
Dp	64	TGTGTCCTCGACAGAGACTTCCACAGATTTGTGTTATGACAGAGGGTGGAGATCCCTAC	123
QY	121	TGCACAGCTGCGCTCCTCGCAGGTACAAAAGACGTGGGGCCACCAATATGTCAAGT	180


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Db 124 TGCACAGCCTGCCCCCTCCGAGGTACAAAAGAGCTGGGGCCACACACAGATGTGACAGT 183
Oy 181 TGCATACCCGTGTGTGCATCAATCGTGTTCAGAAAGTCACTGCACAGCTACCTTAAT 240
Db 184 TGCATACCCGTGTGTGCATCAATCGTGTTCAGAAAGTCACTGCACAGCTACCTTAAT 243
Oy 241 GCTGTCTGTGGGAGCTGTGTGGCCAGGTTCTACCGAAAGACGCAATTGGAGGCTGGAC 300
Db 244 GCCTGTGTGGGAGCTGTGTGGCCAGGTTCTACCGAAAGACGCAATTGGAGGCTGGAC 303
Oy 301 GACCAAGAGTGCATCCCGTGCACGAAGACACCCCACTCTGAGTTCAATGTGCTTC 360
Db 304 GACCAAGAGTGCATCCCGTGCACGAAGACACCCCACTCTGAGTTCAATGTGCTTC 363
Oy 361 CAGTTGAGCTTAGTGGAGGAGATGACCCACAGTCCCTCCTAGAGGCCACACTTGT 420
Db 364 CAGTTGAGCTTAGTGGAGGAGATGACCCACAGTCCCTCCTAGAGGCCACACTTGT 423
Oy 421 GCACTGGTGAAGACCTGTGATGTGTTTACCTGGCCCTTCTGGGGCTTCTTCTC 480
Db 424 GCACTGGTGAAGACCTGTGATGTGTTTACCTGGCCCTTCTGGGGCTTCTTCTC 483
Oy 481 TACTGACAGAGTCTTCTCAACAGACATTTGCCAGCT-----GAGGTTTGTGCAATT 534
Db 484 TACTGACAGAGTCTTCTCAACAGACATTTGCCAGCTTTTGTGCAAGTTT 543
Oy 535 GAGGCTGATATAAACACAAAGAGAGATCTCTTCCCGTGCACCCGCAAGAGAGACC 594
Db 544 GAGGCTGATATAAACACAAAGAGAGATCTCTTCCCGTGCACCCGCAAGAGAGACC 603
Oy 595 AGTCTGAGTCCCAAGT 611
Db 604 AGTCTGAGTCCCAAGT 620

RESULT 9
AAC63991
ID AAC63991 standard; cDNA; 905 BP.
XX AAC63991;
AC AAC63991;
XX
DT 14-FEB-2001 (first entry)
DE Human TNFR homologue clone DNA98853 cDNA.
XX
KW Human; TNFR homologue; tumour necrosis factor receptor; DNA98853;
KW apoptosis; NF-kappa-B activation; proinflammatory response;
KW autoimmune response; modulation; antibody; FDA-A2 inhibition;
KW gene mapping; antisense therapy; gene therapy; ATCC 203906; ss.
XX
OS Homo sapiens.
XX
PN WO20061757-A1.
XX
PD 19-OCT-2000.
XX
PE 12-APR-2000; 2000WO-US09699.
XX
PR 12-APR-1999; 99US-0128849.
XX
PA (GETH ) GENENTECH INC.
XX
PI Goddard A, Pan J, Yan M;
XX
DR P-PSDB; AAB29533.
XX
DR P-PSDB; AAB29533.
XX
PT New isolated nucleic acid encoding a tumor necrosis factor homolog for
PT modulating apoptosis, NF-kappa-B activation, pro-inflammatory or
PT autoimmune response in mammalian cells -
XX
PS Claim 2; Fig 1; 82bp; English.
XX
```

```
CC The invention relates to the human tumour necrosis factor receptor
CC (TNFR) homologue DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
CC encoding them (AAC63991, AAC63992), and to the complements (AAC63992,
CC AAC63994) of nucleic acids encoding the TNFR homologues. The invention
CC also relates to vectors and host cells comprising DNA98853 or DNA101848
CC nucleic acids, fusion proteins comprising the DNA98853 or DNA101848
CC proteins, antibodies against the DNA98853 or DNA101848 proteins,
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CC invention further encompasses a method of modulating apoptosis.
CC NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
CC autoimmune response using the DNA98853 or DNA101848 proteins, and a
CC method of inhibiting or neutralising EDA-A2 protein biological activity
CC in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
CC DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
CC NF-kappa-B activation, proinflammatory or autoimmune responses in
CC mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
CC antibodies) can be used to inhibit or neutralise EDA-A2 protein
CC biological activity in mammalian cells. DNA98853 and DNA101848
CC nucleic acids can be used as hybridisation probes in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, and in gene
CC therapy. The present sequence represents cDNA encoding DNA98853 (ATCC
CC 203906).
CC
XX
SQ
Sequence 905 BP; 210 A; 260 C; 240 G; 195 T; 0 other:
Query Match 85.6%; Score 593.4; DB 22; Length 905;
Best local Similarity 98.9%; Pred. No. 5,5e-168;
Matches 610; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
Oy 1 ATGATTCGCAAGAAATAGTACTGGGAGCCAGCTGTGACCTGCAACGG 60
Db 4 ATGATTCGCAAGAAATAGTACTGGGAGCCAGCTGTGACCTGCAACGG 63
Oy 61 TGTGGTCTGAGACAGAGAGATATGCAAGATTTGTTATGAGAGGTGAGATGCTTAC 120
Db 64 TGTGGTCTGAGACAGAGAGATATGCAAGATTTGTTATGAGAGGTGAGATGCTTAC 123
Oy 121 TGCACAGCTGCGCCCTCCGAGGTACAAAAGAGCTGGGGCCACCAATGTGACAGT 180
Db 124 TGCACAGCTGCGCCCTCCGAGGTACAAAAGAGCTGGGGCCACCAATGTGACAGT 183
Oy 181 TGCATACCTGTGCTCATCATATCGTGTTCAGAAAGTGCATGACAGTACCTTAAT 240
Db 184 TGCATACCTGTGCTCATCATATCGTGTTCAGAAAGTGCATGACAGTACCTTAAT 243
Oy 241 GCTGTCTGTGGGAGCTGTGTGGCCAGGTTCTACCGAAAGACAGCATTTGAGGCTGCAG 300
Db 244 GCTGTCTGTGGGAGCTGTGTGGCCAGGTTCTACCGAAAGACAGCATTTGAGGCTGCAG 303
Oy 301 GACCAAGAGTGCATCCCGTGCACGAAGACACCCCACTCTGAGTTCAATGTGCTTC 360
Db 304 GACCAAGAGTGCATCCCGTGCACGAAGACACCCCACTCTGAGTTCAATGTGCTTC 363
Oy 361 CAGTTGAGCTTAGTGGAGGAGATGACCCACAGTCCCTCCTAGAGGCCACACTTGT 420
Db 364 CAGTTGAGCTTAGTGGAGGAGATGACCCACAGTCCCTCCTAGAGGCCACACTTGT 423
Oy 421 GCACTGGTGAAGACCTGTGATGTGTTTACCTGGCCCTTCTGGGGCTTCTTCTC 480
Db 424 GCACTGGTGAAGACCTGTGATGTGTTTACCTGGCCCTTCTGGGGCTTCTTCTC 483
Oy 481 TACTGACAGAGTCTTCTCAACAGACATTTGCCAGCT-----GAGGTTTGTGCAATT 534
Db 484 TACTGACAGAGTCTTCTCAACAGACATTTGCCAGCTTTTGTGCAAGTTT 543
Oy 535 GAGGCTGATATAAACACAAAGAGAGATCTCTTCCCGTGCACCCGCAAGAGAGACC 594
Db 544 GAGGCTGATATAAACACAAAGAGAGATCTCTTCCCGTGCACCCGCAAGAGAGACC 603
Oy 595 AGTCTGAGTCCCAAGT 611
Db 604 AGTCTGAGTCCCAAGT 620
```



```
RESULT 10
AAC63992/c
ID AAC63992 standard; cDNA; 905 BP.
XX
AC AAC63992:
XX
DT 14-FEB-2001 (first entry)
XX
DE Human TNFR homologue clone DNA98853 cDNA complement.
XX
KW Human; TNFR homologue; tumour necrosis factor receptor; DNA98853;
KW apoptosis; NF-kappa-B activation; proinflammatory response;
KW autoimmune response; modulation; antibody; EDA-A2 inhibition;
KW gene mapping; antisense therapy; gene therapy; ATCC 203906; ss.
XX
OS Homo sapiens.
XX
PN WO200061757-A1.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000MO-US09699.
XX
PR 12-APR-1999; 990S-0128849.
XX
PA (GETH ) GENENTECH INC.
XX
PI Goddard A, Pan J, Yan M;
XX
DR WPI; 2001-070561/08.
XX
P-PSDB; AAB29533.
XX
PT New isolated nucleic acid encoding a tumor necrosis factor homolog for
PT modulating apoptosis, NF-kappaB activation, pro-inflammatory or
PT autoimmune response in mammalian cells -
XX
PS Claim 2; Fig 1; 82pp; English.
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CC The invention relates to the human tumour necrosis factor receptor
CC (TNFR) homologues DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
CC encoding them (AAC63991, AAC63993), and to the complements (AAC63992,
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CC invention further encompasses a method of modulating apoptosis,
CC NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
CC autoimmune response using the DNA98853 or DNA101848 proteins, and a
CC method of inhibiting or neutralising EDA-A2 protein biological activity
CC in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
CC DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
CC NF-kappa-B activation, proinflammatory or autoimmune responses in
CC mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
CC antibodies) can be used to inhibit or neutralise EDA-A2 protein
CC biological activity in mammalian cells. DNA98853 and DNA101848
CC nucleic acids can be used as hybridisation probes in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, and in gene
CC therapy. The present sequence represents the complement of the cDNA
CC encoding DNA98853 (ATCC 203906).
XX
SQ Sequence 905 BP; 195 A; 240 C; 260 G; 210 T; 0 other;
XX
Query Match 85.6%; Score 593.4; DB 22; Length 905;
Best Local Similarity 98.9%; Pred. No. 5,5e-168;
Matches 610; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
XX
OY 1 ATGATTTGCCAAGAAATGACTAGGACCAATGGGAGCGTGTGCTACCTGCCACGG 60
DB 902 ATGATTTGCCAAGAAATGACTAGGACCAATGGGAGCGTGTGCTACCTGCCACGG 843
OY 61 TGTGTCCTGACAGAGCTATCCAAAGATTTGTGTTATGAGAGGCTGAGATGCTTAC 120
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DB 842 TGTGTCCTGACAGAGCTATCCAAAGATTTGTGTTATGAGAGGCTGAGATGCTTAC 783
OY 121 TGCACAGCCTGCTCCTCCTCGAGGTACAAAAGCAGCTGGGGCCACCAAAATGTCAGAGT 180
DB 782 TGCACAGCCTGCTCCTCCTCGAGGTACAAAAGCAGCTGGGGCCACCAAGATGTCAGAGT 723
OY 181 TGCATCACTGCTGCTGATCATCATGCTGTGTAGAAAGTCAACATGACAGCTACTCTAAT 240
DB 722 TGCATCACTGCTGCTGATCATCATGCTGTGTAGAAAGTCAACATGACAGCTACTCTAAT 663
OY 241 GCTGTCGTGGGAGCTGTTTCCAGGTTTACCGAAAAGACACCATTTGAGGCTGACAG 300
DB 662 GCTGTCGTGGGAGCTGTTTCCAGGTTTACCGAAAAGACACCATTTGAGGCTGACAG 603
OY 301 GACCAAGAGTCAATCCGTCGACAGACAGACCCCACTCTGAGTTCAATGTGCTTC 360
DB 602 GACCAAGAGTCAATCCGTCGACAGACAGACCCCACTCTGAGTTCAATGTGCTTC 543
OY 361 CAGTTGAGCTTACGTGAGAGGATGACACCCACAGTGGCCCCCTCAGAGAGCCACTTGT 420
DB 542 CAGTTGAGCTTACGTGAGAGGATGACACCCACAGTGGCCCCCTCAGAGAGCCACTTGT 483
OY 421 GCAGTGTGAGCAGCCTGCTAGTGTGTTACCTGGGCTTCTGGGAGCTTCTTCTC 480
DB 482 GCAGTGTGAGCAGCCTGCTAGTGTGTTACCTGGGCTTCTGGGAGCTTCTTCTC 423
OY 481 TACTGCAAGCAGTCTTCAACAGACATTCACAGGT-----GGAGTTTGTCTCAGTTT 534
DB 422 TACTGCAAGCAGTCTTCAACAGACATTCACAGGTACAGAGGTTTGTCTCAGTTT 363
OY 535 GAGGCTGATTAACAGAAAGAGAAATCTCTTCCCGCCAGCCAGCAAGAGAAC 594
DB 362 GAGGCTGATTAACAGAAAGAGAAATCTCTTCCCGCCAGCCAGCAAGAGAAC 303
OY 595 AGTGCTGAGTCCCAAGT 611
DB 302 AGTGCTGAGTCCCAAGT 286
XX
RESULT 11
AAA47453
ID AAA47453 standard; cDNA; 1550 BP.
XX
AC AAA47453:
XX
DT 20-OCT-2000 (first entry)
XX
DE Human TANGO 140-1 coding sequence.
XX
KW TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW graft versus-host diseases; rheumatoid arthritis; psoriasis;
KW inflammatory bowel disease; septic shock; ulcerative colitis;
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver
KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;
KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;
KW systemic lupus erythematosus; transgenic animal; diagnosis;
KW prognosis; prophylactic; therapeutic; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..622
FT /tag= a
FT /product= TANGO 140-1
XX
PN WO200039284-A1.
XX
PD 06-JUL-2000.
XX
PF 23-DEC-1999; 99MO-US31025.
XX
PR 30-DEC-1998; 98US-0223546.
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XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Holtzman DA;
PI
XX WPI: 2000-465743/40.
DR
DR P-PSDB; AAB01420.
XX
PT Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,
PT 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases
XX
XX Claim 1; Fig 2; 209pp; English.
XX
CC Nucleic acids encoding TANGO polypeptides are useful as modulating
CC agents for regulating cellular processes like asthma, graft
CC versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory
CC bowel disease, septic shock, ulcerative colitis, Crohn's disease,
CC chronic myelogenous leukemia, cancer, liver disease, Hodgekin's
CC disease, osteoarthritis, Lyme's disease, cachexia and autoimmune
CC diseases e.g. myasthenia gravis, autoimmune diabetes and systemic
CC lupus erythematosus. The nucleic acids are also useful for producing
CC transgenic animals and the TANGO polypeptides themselves. Partial
CC TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in
CC forensic biology, for diagnostic assays, prognostic assays,
CC pharmacogenomics and for monitoring clinical trials. TANGO
CC polypeptides are suitable for both prophylactic and therapeutic
CC methods for treating a subject at risk of a disorder or having a
CC disorder associated with aberrant TANGO expression. A wide range
CC of cellular disorders can be treated.
XX
XX Sequence 1550 BP; 452 A; 329 C; 392 G; 377 T; 0 other:
SQ
Query Match 74.7%; Score 518; DB 21; Length 1550;
Best Local Similarity 100.0%; Pred. No. 3,1e-145;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGGATTGCCAAGAAATAGTACTGAGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG 60
DB 26 ATGGATTGCCAAGAAATAGTACTGAGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG 85
OY 61 TGTGTCCTGACAGAGAGCTATCCAAAGATTGTGTTATGAGAGGGTGGAGATGCCCTAC 120
DB 86 TGTGTCCTGACAGAGAGCTATCCAAAGATTGTGTTATGAGAGGGTGGAGATGCCCTAC 145
OY 121 TGCACAGCTGCCCTCCTCGCAGGTACAAAGACACTGGGGCCACCACCAATGTAGACT 180
DB 146 TGCACAGCTGCCCTCCTCGCAGGTACAAAGACACTGGGGCCACCACCAATGTAGACT 205
OY 181 TGCATCACCTGCTGTCTATCAATGCTGTTCAGAAAGTCAACTGCACAGCTCACTTAAT 240
DB 206 TGCATCACCTGCTGTCTATCAATGCTGTTCAGAAAGTCAACTGCACAGCTCACTTAAT 265
OY 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGCGCTGCAG 300
DB 266 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTACCGAAAGACAGCATTTGGAGCGCTGCAG 325
OY 301 GACCAAGAGTGTATCCCGTGGCAGCAAGACAGACCCCACTCTGAGGTTTAATGTGCTTC 360
DB 336 GACCAAGAGTGTATCCCGTGGCAGCAAGACAGACCCCACTCTGAGGTTTAATGTGCTTC 385
OY 361 CAGTTGAGCTTGTGAGGAGATGACACCAAGTCCGCCCTCAGAGAGCCACACTTGT 420
DB 386 CAGTTGAGCTTGTGAGGAGATGACACCAAGTCCGCCCTCAGAGAGCCACACTTGT 445
OY 421 GCACGTGTGAGAGCGCTGTAGTGTGTTTACCTGGCCCTTCTCGGGCTCTTCTTCCTC 480
DB 446 GCACGTGTGAGAGCGCTGTAGTGTGTTTACCTGGCCCTTCTCGGGCTCTTCTTCCTC 505
OY 481 TACTGCAAGCAATTTCTTAACAGACATTTGCCAGCTGG 518
DB 506 TACTGCAAGCAATTTCTTAACAGACATTTGCCAGCTGG 543
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RESULT 12
AAS05960
ID AAS05960 standard; cDNA; 891 BP.
XX
XX AAS05960;
AC
XX
XX 07-SEP-2001 (first entry)
DE
XX Degenerate cDNA sequence for human UMLR variant #1.
XX
XX Human; uterine myometrium leiomyoma receptor; UMLR; znfr11;
KW tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200130850-A1.
XX
XX 03-MAY-2001.
XX
XX 23-OCT-2000; 2000WO-US29304.
XX
XX 22-OCT-1999; 99US-0160880.
XX
XX 02-NOV-1999; 99US-0163215.
XX
XX 17-JUL-2000; 2000US-0218769.
XX
XX 01-AUG-2000; 2000US-0222221.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Xu W, Lofton-Day CE, Henne R, Presnell SR, Yao Y, Novak JF;
PI Foster DC, Yee DP;
XX
XX WPI: 2001-300488/31.
XX
XX uterine myometrium leiomyoma receptor polypeptides and polynucleotides
XX for modulating inflammation, tumour growth, metastasis, cellular
XX maturation, detecting modulators and as diagnostic indicators of cancer
XX
XX Example 12; Page 133; 148pp; English.
XX
XX The present sequence represents a degenerate cDNA sequence for human
XX uterine myometrium leiomyoma receptor (UMLR) variant #1. UMLR is a novel
XX member of the tumour necrosis factor receptor (TNFR) family. The UMLR
XX (also known as znfr11) gene maps to chromosome Xq11-q12. Amino acid
XX residues of UMLR involved in ligand binding, consisting of residues 1-X
XX (where X is 129-136) are useful for inhibiting the quantity of lung,
XX breast carcinoma, melanoma, osteosarcoma or lymphoma cells expressing
XX UMLR protein. UMLR polypeptides or its fragments are useful
XX diagnostically or therapeutically for identifying tumour cells in uterus
XX leiomyoma and lung cancer, for promoting wound healing, and for generating
XX vaccines for cancer therapy. They are also useful for studying cell-cell
XX interactions, apoptosis, fertilisation, development, immune recognition,
XX growth control, tumour suppression and embryo maturation in vitro and in
XX vivo, and for treating disorders associated with them. UMLR is also
XX useful for identifying inhibitors of its activity, and for preparing
XX antibodies which can be used to detect UMLR expression. UMLR
XX polynucleotide sequences are useful as probes or primers as diagnostic
XX indicators of cancer and for gene therapy.
XX
XX Sequence 891 BP; 141 A; 105 C; 150 G; 112 T; 383 other:
SQ
Query Match 64.4%; Score 446.6; DB 22; Length 891;
Best Local Similarity 58.6%; Pred. No. 6.7e-124;
Matches 360; Conservative 147; Mismatches 107; Indels 0; Gaps 0;
OY 1 ATGGATTGCCAAGAAATAGTACTGAGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG 60
DB 1 ATGGATTGCCAAGAAATAGTACTGAGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG 60
OY 61 TGTGTCCTGACAGAGAGCTATCCAAAGATTGTGTTATGAGAGGGTGGAGATGCCCTAC 120
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Db 61 TGYGNCNGNCNGNCARGARATYTWMSNAARATYTGNGNTAYGNGAGGAGGAGCMTAY 120
121 TGCACACCCCTCCTCCTCCGAGGTACAAAAGACAGTCGGCCACCAACAAATGTACAGT 180
122 TGYACNCNNTGYCCNCNMGMNGNTAYAAARMSNMTGGGNCAYCAAAATGTGCARSN 180
181 TGCATCACCTGTGCTGCATCATCATCGTGTTCAGAAAGTCAACTGCACAGCTACTTAAT 240
181 TGYATTHACNTGYCGCNGTNATHAAAYMGNTNCARARAGTNAAYTACNGCNAACNMSNAY 240
241 GCTGTCTGTGGGAGCTGTTGGCCAGGTTCACCGAANAAGACACCATTTGGAGGCTGCAG 300
241 GCNNTNTGYGNGAYTGYTTCNCNMGNTTYTAYMGNAARACNMGNATHGNGGNTTCAR 300
301 GACCAAGAGTGCATCCCTGCAGACAGACAGACCCCTCTGTGAGTTCAATGTGCCTC 360
301 GAYCARARATGYATHCNCNTGYACAAARACARACNCNMSNGARGTNCARTGTGCTT 360
361 CAGTTGAGCTTGTAGTGAGGAGATGCACCAAGTGCCTCCCTCAGAGGCCACACTTGT 420
361 CARYTMSNNTNGTNGARCGAGCAGCNCNACNGTNCNCNCARGARCGACACNTNGTN 420
421 GCACGTGTGAGCAGCCCTGCTAGTGTGTTCACCTGGCCTTCTGGGGCTCTTCTCCTC 480
421 GCNNTNTGYGNGAYTGYTTCNCNMGNTTYTAYMGNAARACNMGNATHGNGGNTTYTN 480
481 TACTGCACAGTTCCTTCACACAGACATTCAGAGCTGAGGCTTGCAGATTCAGAGCT 540
481 TATYTAARARARTTYYTAAAYMGNCATYTCARMGNGNGNNTYTNCAATYTGARCN 540
541 GATPAAACAGCAAAAGAGGAATCTCTTCCCGTGCACCCAGCAAGAGACCATGCT 600
541 GAYAAARACNCNNAARGARARMSNTYTCNCGTNCNCNMSNAARGARACMWSNGCN 600
OY 601 GAGTCCCAACTCTC 614
Db 601 GARMSNCAAGTMS 614

RESULT 13
AAS05945
AAS05945 standard; cDNA; 807 BP.
XX
AC AAS05945;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human uterine myometrium leiomyoma receptor (UMLR) degenerate sequence.
XX
KW Human: uterine myometrium leiomyoma receptor; UMLR; ztf11;
KW tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
PN W0200130850-A1.
XX
PD 03-MAY-2001.
XX
PE 23-OCT-2000; 2000MO-US29304.
XX
PR 22-OCT-1999; 99US-0160880.
PR 02-NOV-1999; 99US-0163215.
PR 17-JUL-2000; 2000US-0218769.
PR 01-AUG-2000; 2000US-0222221.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Xu W, Lofton-Day CE, Henne R, Presnell SR, Yao Y, Novak JE;
PI Foster DC, Yee DP;
XX
```

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DR WPI: 2001-300488/31.
XX
PT uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT for modulating inflammation, tumour growth, metastasis, cellular
PT maturation, detecting modulators and as diagnostic indicators of cancer
PT
XX
PS Disclosure: Page 117-118; 148pp; English.
XX
CC The present sequence represents a degenerate sequence encoding for a
CC novel human uterine myometrium leiomyoma receptor (UMLR) which is a
CC member of the tumour necrosis factor receptor (TNFR) family. The UMLR
CC (also known as ztnfr1) gene maps to chromosome Xq11-q12. Amino acid
CC residues of UMLR involved in ligand binding, consisting of residues 1-X
CC (where X is 129-136) are useful for inhibiting the quantity of lung,
CC breast carcinoma, melanoma, osteosarcoma or lymphoma cells expressing
CC UMLR protein. UMLR polypeptides or its fragments are useful
CC diagnostically or therapeutically for identifying tumour cells in uterus
CC melanoma and lung cancer, for promoting wound healing, and for generating
CC vaccines for cancer therapy. They are also useful for studying cell-cell
CC interactions, apoptosis, fertilisation, development, immune recognition,
CC growth control, tumour suppression and embryo maturation in vitro and in
CC vivo, and for treating disorders associated with them. UMLR is also
CC useful for identifying inhibitors of its activity, and for preparing
CC antibodies which can be used to detect UMLR expression. UMLR
CC polynucleotide sequences are useful as probes or primers as diagnostic
CC indicators of cancer and for gene therapy.
XX
SQ Sequence 807 BP; 125 A; 93 C; 142 G; 102 T; 345 other;
```

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Query Match 64.4%; Score 446.4; DB 22; Length 807;
Best Local Similarity 55.4%; Pred. No. 7.3e-124;
Matches 370; Conservative 156; Mismatches 142; Indels 0; Gaps 0;
```

```
OY 1 ATGGATTGCCAAGAAATGACTGCGACCAATGGGAGCGTGTTCACCTGCCAAGC 60
1 ATGGATYGCARARAAATGATYATGGAYCARTGGAGCNGMONTGYTACNTGYCARMG 60
Db 1 TGTGGTCTGTGAGCAGGAGATTCACCAAGATTTGTGTATGAGAGGCTGAGATGCTAC 120
61 TGTGGNCNCNGNCARGARATYTWMSNAARATYTGNGNTAYGNGAGGAGGAGCMTAY 120
OY 121 TGCACACCCCTCCTCCTCCGAGGTACAAAAGACAGTGCCTCCCTCAGAGGCCACACTTGT 180
121 TGYACNCNNTGYCCNCNMGMNGNTAYAAARMSNMTGGGNCAYCAAAATGTGCARSN 180
OY 181 TGCATCACCTGTGCTGCATCATCATCGTGTTCAGAAAGTCAACTGCACAGCTACTTAAT 240
181 TGYATTHACNTGYCGCNGTNATHAAAYMGNTNCARARAGTNAAYTACNGCNAACNMSNAY 240
OY 241 GCTGTCTGTGGGAGCTGTTGGCCAGGTTCACCGAANAAGACACCATTTGGAGGCTGCAG 300
241 GCNNTNTGYGNGAYTGYTTCNCNMGNTTYTAYMGNAARACNMGNATHGNGGNTTCAR 300
OY 301 GACCAAGAGTGCATCCCTGCAGACAGACAGACCCCTCTGTGAGTTCAATGTGCCTC 360
301 GAYCARARATGYATHCNCNTGYACAAARACARACNCNMSNGARGTNCARTGTGCTT 360
OY 361 CAGTTGAGCTTGTAGTGAGGAGATGCACCAAGTGCCTCCCTCAGAGGCCACACTTGT 420
361 CARYTMSNNTNGTNGARCGAGCAGCNCNACNGTNCNCNCARGARCGACACNTNGTN 420
OY 421 GCACGTGTGAGCAGCCCTGCTAGTGTGTTCACCTGGCCTTCTGGGGCTCTTCTCCTC 480
421 GCNNTNTGYGNGAYTGYTTCNCNMGNTTYTAYMGNAARACNMGNATHGNGGNTTYTN 480
OY 481 TACTGCACAGTTCCTTCACACAGACATTCAGAGCTGAGGCTTGCAGATTCAGAGCT 540
481 TATYTAARARARTTYYTAAAYMGNCATYTCARMGNGNGNNTYTNCAATYTGARCN 540
OY 541 GATPAAACAGCAAAAGAGGAATCTCTTCCCGTGCACCCAGCAAGAGACCATGCT 600
541 GAYAAARACNCNNAARGARARMSNTYTCNCGTNCNCNMSNAARGARACMWSNGCN 600
Db
```

Oy		601 GAGGCCCAAGCTCTGTGGCCCGGACGCCTTGCCAGTTGTCCTGACTCATT	660 : :
Dd	601	GARMSNCARGARWSMTTYTACNATGGCWNSTNGTAGCNMSGARNCSAIVMSCAITGGGTN	: :
Oy	661	CCTATACC 668	:
Dd	661	CAYSMNC 668	:
	RESULT 14		
	AAAA7454		
	AAAA7454 standard; cDNA; 3385 BP.		
Xx	AAA47454;		
Ac			
Xx	20-OCT-2000 (first entry)		
Dt			
Xx	Human TANGO 140-2 coding sequence.		
De			
Xx	TANGO: 128: 140: 197: 212: 213: 224: 239: modulating agent; asthma; graft versus host diseases; rheumatoid arthritis; psoriasis; - inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthenia gravis; autoimmune systemic lupus erythematosus; transgenic animal; diagnosis; prognosis; prophylactic; therapeutic; human; ds.		
Kw			
Km			
Os	Homo sapiens.		
Xx			
Fh	Key Location/Qualifiers		
Ff	CDS 1..594		
Ef	/tag= a		
Ft	/product= TANGO 140-2		
Pt			
Xx			
Xn	WO200039284-A1.		
Pn			
Pd	06-JUL-2000.		
Xx			
Pf	23-DEC-1999; 99WO-US31025.		
Xx			
Pp	30-DEC-1998; 98US-0223546.		
Xx			
Pa	(MILL-) MILLENNIUM PHARM INC.		
Xx			
Pi	Holtzman DA;		
Dr	WPI: 2000-465743/40.		
Dd	P-PsDB; AAB01421.		
Xx			
Pt	Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases		
Ps	Claim 1; Fig 3; 209pp; English.		
Xx			
Cc	Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthenia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.		

XX	Sequence	3385 BP; 915 A; 801 C; 718 G; 951 T; 0 other:
QY	Query Match	61.7%; Score 427.4; DB 2L; Length 3385;
Db	Best Local Similarity	99.8%; Pred. No. 7e-118;
Matches 428:	Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1	ATGATATGCCCAAGAAATAGTACTTGTGGGACCAATGGGACGGGTGTGCACCTGCCAACGG 60
Db	67	ATGATGTTCCCAAGAAATAGTACTTGTGGGACCAATGGGACGGGTGTGCACCTGCCAACGG 126
QY	61	TGTGTCCTGTGCACAGAGACTATCCAAAGATTGTGTTATGGAGAGGTGGAGATGCTTAC 120
Db	127	TGTGTCCTGTGCACAGAGACTATCCAAAGATTGTGTTATGGAGAGGTGGAGATGCTTAC 186
QY	121	TGCACAGCCTGGCCCTCTCGACAGTATCAAAAGCAGCTGGGGCCACCACCAATGTCCAGAGT 180
Db	187	TGCACAGCCTGGCCCTCTCGACAGTATCAAAAGCAGCTGGGGCCACCACCAATGTCCAGAGT 246
QY	181	TGCATCACCCTGTGCTGTCTATCATATGTTGTTCAGAAAGTTAACTGCACACTTACTTAAAT 240
Db	247	TGCATCACCCTGTGCTGTCTATCATATGTTGTTCAGAAAGTTAACTGCACACTTACTTAAAT 306
QY	241	GCTGTCCTGGGGGACCTGTTTGGCCAGGTCTTCCCGAAGACGCACTTGGAGGCTCGAC 300
Db	307	GCTGTCCTGGGGGACCTGTTTGGCCAGGTCTTCCCGAAGACGCACTTGGAGGCTCGAC 366
QY	301	GACCAAGAGTGCATCCCGTGCACGAGACGACCCCCACCTGTGAGGTCAATGTGCTTTC 360
Db	367	GACCAAGAGTGCATCCCGTGCACGAGACGACCCCCACCTGTGAGGTCAATGTGCTTTC 426
QY	361	CAGTTGAGCTTATGTGAGGACAGATGCACCCACAGTCCGCCCTGAGAGGCGACACTTGT 420
Db	427	CAGTTGAGCTTATGTGAGGACAGATGCACCCACAGTCCGCCCTGAGAGGCGACACTTGT 486
QY	421	GCACGTGAGTG 429
Db	487	GCACGTGTTG 495
RESULT 15		
AA0505973		
XX	AA0505973 standard; DNA; 1081 BP.	
XX	AA0505973;	
XX	07-SEP-2001 (first entry)	
DE	Expression vector pZP72 insert sequence containing ztnfr11/TNFR1 chimera.	
XX	Mouse; uterine myometrium leiomyoma receptor; UMLR; ztnfr11;	
KM	tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;	
KM	breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;	
KM	gene therapy; human; mutant; ds.	
XX	Chimeric - Mus sp.	
OS	Chimeric - Homo sapiens.	
OS	Synthetic.	
XX	WO200130850-A1.	
XX	03-MAY-2001.	
PD	23-OCT-2000; 2000MO-US29304.	
XX	22-OCT-1999; 99US-0160880.	
PR	02-NOV-1999; 99US-0163215.	
PR	17-JUL-2000; 2000US-0218769.	
PR	01-AUG-2000; 2000US-0222221.	
XX	(ZYMO) ZYMOGENETICS INC.	
PA		
XX	Xu W, Lofton-Day CE, Henne R, Presnell SR, Yao Y, Novak JE;	

PI Foster DC, Yee DP;
XX
DR WPI: 2001-300488/31.
XX

PT Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT for modulating inflammation, tumour growth, metastasis, cellular
PT maturation, detecting modulators and as diagnostic indicators of cancer
PT

XX
PS Example 14; Page 143-144; 148pp: English.
XX

CC The present sequence for expression vector p2P7Z insert sequence
CC contains the sequence for a ztnfr1/TNFR1 chimera and the K2159/m14
CC reporter gene sequence. Human ztnfr1 or UMLR (uterine myometrium
CC leiomyoma receptor is a novel member of the tumour necrosis factor
CC receptor (TNFR) family. The UMLR (also known as ztnfr1) gene maps
CC to chromosome Xq11-q12. Amino acid residues of UMLR involved in ligand
CC binding, consisting of residues 1-X (where X is 129-136) are useful for
CC inhibiting the quantity of lung, breast carcinoma, melanoma, osteosarcoma
CC or lymphoma cells expressing UMLR protein. UMLR polypeptides or its
CC fragments are useful diagnostically or therapeutically for identifying
CC tumour cells in uterus melanoma and lung cancer, for promoting wound
CC healing, and for generating vaccines for cancer therapy. They are also
CC useful for studying cell-cell interactions, apoptosis, fertilisation,
CC development, immune recognition, growth control, tumour suppression and
CC embryo maturation in vitro and in vivo, and for treating disorders
CC associated with them. UMLR is also useful for identifying inhibitors of
CC its activity, and for preparing antibodies which can be used to detect
CC UMLR expression. UMLR polynucleotide sequences are useful as probes or
CC primers as diagnostic indicators of cancer and for gene therapy.
XX

SQ Sequence 1081 BP; 248 A; 311 C; 306 G; 216 T; 0 other;

Query Match 59.6%; Score 413.2; DB 22; Length 1081;

Best Local Similarity 99.3%; Pred. No. 7.8e-114;

Matches 415; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ATGGATTGCCAAGAAATGAGTACTGAGCAATGGGAGCGTGTGCTACCTGCCAAGCG 60
DB 1 ATGGATTGCCAAGAAATGAGTACTGAGCAATGGGAGCGTGTGCTACCTGCCAAGCG 60
OY 61 TGTGTCCTGGAGAGAGCTATCCAAAGATTGTGTTATGAGAGGGTGGAGATGCCTAC 120
DB 61 TGTGTCCTGGAGAGAGCTATCCAAAGATTGTGTTATGAGAGGGTGGAGATGCCTAC 120
OY 121 TGCACAGCCTGCCCTCCTGCGAGGTACAAAGAGAGCTGGGGCCACCAATGTCAAGAT 180
DB 121 TGCACAGCCTGCCCTCCTGCGAGGTACAAAGAGAGCTGGGGCCACCAATGTCAAGAT 180
OY 181 TGCATACCTGTGCTCATCATCTGTTTCAAGAGTCAATGCAAGCTACCTCTAAT 240
DB 181 TGCATACCTGTGCTCATCATCTGTTTCAAGAGTCAATGCAAGCTACCTCTAAT 240
OY 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTTACCGAAGACACGCAATGGAGGCTGCAG 300
DB 241 GCTGTCTGTGGGAGCTGTTTGGCCAGGTTCTTACCGAAGACACGCAATGGAGGCTGCAG 300
OY 301 GACCAAGAGTGCATCCGTGGACAGAGACCCCACTCTAGAGTTCAATGTGCTTC 360
DB 301 GACCAAGAGTGCATCCGTGGACAGAGACCCCACTCTAGAGTTCAATGTGCTTC 360
OY 361 CAGTTAGGCTTAGTGAGGAGAGATGCACCCACAGTCCCTCAGAGGCGCACACTTG 418
DB 361 CAGTTAGGCTTAGTGAGGAGAGATGCACCCACAGTCCCTCAGAGGCGCACACTTG 418

Search completed: October 27, 2002, 01:37:17
Job time : 250 secs

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